

DATE: 04/30/98 TIME: 15:19:53

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This Raw Listing contains the General Information Section and up to the first 5 pages.

1 2	SEQUENCE LISTING ENTE
3 4	(1) General Information:
5 6 7 8	(i) APPLICANT: Gerard, Gary F. Smith, Michael D. Chatterjee, Deb K.
9 10 11	(ii) TITLE OF INVENTION: Compositions and Methods for Reverse Transcription of Nucleic Acid Molecules
12 13	(iii) NUMBER OF SEQUENCES: 23
14 15 16 17 18 19 20 21	(iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. (B) STREET: 1100 New York Avenue, Suite 600 (C) CITY: Washington (D) STATE: DC (E) COUNTRY: USA (F) ZIP: 20005
22 23 24 25 26 27	 (V) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28 30 31 32	<pre>(vi) CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: (To be assigned) (B) FILING DATE: (Herewith) (C) CLASSIFICATION:</pre>
33 34 35 36 37	<pre>(Vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: US 60/049,874 (B) FILING DATE: 17-JUN-1997 (C) CLASSIFICATION:</pre>
38 39 40 41	(Vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: US 60/044,589 (B) FILING DATE: 22-APR-1997
42 43 44 45 46	(viii) ATTORNEY/AGENT INFORMATION: (A) NAME: Esmond, Robert W. (B) REGISTRATION NUMBER: 32,893 (C) REFERENCE/DOCKET NUMBER: 0942.4330002

RAW SEQUENCE LISTING PATENT APPLICATION US/09/064,057

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(ix) TELECOMMUNICATION INFORMATION: INPUT SET: S25451.raw (A) TELEPHONE: 202-371-2600 (B) TELEFAX: 202-371-2540 (2) INFORMATION FOR SEQ ID NO:1: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: AGGAGACCCA TATGACTGTT GCGCTACATC TGGCT (2) INFORMATION FOR SEQ ID NO:2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: AACGCGACAG GTTAACAGCG CGCAAATCAT GCAG (2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:



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		00 01 CACACAGG TACCCTCTCG AAAAGTTAAA CC	INPUT SET: S25451.raw
	10)3 (2) INFORMATION FOR SEC ID NO. 4	32
	10 10 10 10 10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both	
	11: 11: 11: 11:	1 (ii) MOLECULE TYPE: cDNA 2 3	
	116 117	(NI) DEQUENCE DESCRIPTION, GEO. To	
1000	118 119	CACACACACT CGAGTTATCC AAAAACACACC	
	120 121	(2) INFORMATION FOR SEC ID NO. 5	41
	122 123 124 125 126 127 128 129	(A) LENGTH: 36 bags mark	
	130 131 132 133 134	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
ŭ	135 136	GGACCCACTG TCTTTACCGC GGCCTCCTCA AGCACC	26
	137 138 139 140 141 142 143 144 145 146 147	(2) INFORMATION FOR SEQ ID NO:6: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both (ii) MOLECULE TYPE: cDNA	36
	149 150	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
	151 152	CACACACCC CGGGTTAATA CGCTTGGAAG GTGGC	
		- CGCTTGGAAG GTGGC	35

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DAW SEQUENCE LISTING

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153 154	(2) INFORMATION FOR SEQ ID NO:7:	
155 156 157 158 159 160 161	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both 	
162 163 164 165 166	(ii) MOLECULE TYPE: cDNA	
167 168	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	•
169	CACACACATC ATGACTGTTG CGCTACATCT G	31
170 171	(2) INFORMATION FOR SEQ ID NO:8:	
172 173 174 175 176 177	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both 	
179 180 181 182 183	(ii) MOLECULE TYPE: cDNA	
184 185	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
186 187	CACACAGG TACCCTCTCG AAAAGTTAA	29
188 189	(2) INFORMATION FOR SEQ ID NO:9:	
190 191 192 193 194 195	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both 	
196 197 198 199 200	(ii) MOLECULE TYPE: cDNA	
201 202	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
203	CACACAGA GGAATTCAGT GATGGTGATG GTGATGTGCA AAAAGAGG	48
204 205	(2) INFORMATION FOR SEQ ID NO:10:	

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206	·	
207	(i) SEQUENCE CHARACTERISTICS:	
208	(A) LENGTH: 41 base pairs	
209	(B) TYPE: nucleic acid	
210	(C) STRANDEDNESS: both	
211	(D) TOPOLOGY: both	
212	(5) 101020011 20011	
213	(ii) MOLECULE TYPE: cDNA	
214	(11) Meddeddd IIId. Chw	
215		
216		
217		
218	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
219	(XI) SEGORACE DESCRIPTION: SEQ ID NO:10:	
220	ACTGGAATTC ATGCCAATCC ATCACCATCA CCATCACCCG T	
221	ACIGGRATIC AIGCCAATCC ATCACCATCA CCATCACCCG T	41
222	(2) INFORMATION FOR SEC ID NO.11.	
223	(2) INFORMATION FOR SEQ ID NO:11:	
224	(i) CHOURNER CHARACTER CONT.	
225	(i) SEQUENCE CHARACTERISTICS:	
226	(A) LENGTH: 41 base pairs	
227	(B) TYPE: nucleic acid	
227	(C) STRANDEDNESS: both	
229	(D) TOPOLOGY: both	
230	(ii) NOTEGUED BURD - DATA	
231	(ii) MOLECULE TYPE: cDNA	
231		
232		
233		
234	() CROUENCE PECCETON CE	
236	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
236	ACCIMOMOCA CAMAMOCAMO ACMACAMANA ACCIMONA	
238	ACGTGTCGAC CATATGGATG ACTAGGTGAA ACGGGTGATG G	41
239	(2) INFORMATION FOR GRO IN NO 10	
240	(2) INFORMATION FOR SEQ ID NO:12:	
241	(i) CEQUENCE GUADA CONTRAC	
241	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 71 base pairs	
243	(B) TYPE: nucleic acid	
244	(C) STRANDEDNESS: both	
245	(D) TOPOLOGY: both	
246	AND NOT DESIGN THE THE	
247	(ii) MOLECULE TYPE: cDNA	
248		
249		
250		
251		
252	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
253		
254	ACTGGAATTC ATGCCAATCC ATCACCATCA CCATCACCCG TTTCACCTAG TCATCCATAT	60
255	COTTOO A CO. T.	
256 257	GGTCGACACG T	71
<i>1</i> .3 <i>1</i>		